

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/700,737...DATE: 12/18/96
TIME: 14:31:40

INPUT SET: S14479.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Ponath, Paul D.
Ringler, Douglas J.
Jones, S. Tarran
Newman, Walter
Saldanha, Jos
Bendig, Mary M.

(ii) TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH A4 7
INTEGRIN

(iii) NUMBER OF SEQUENCES: 63

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: Two Militia Drive
(C) CITY: Lexington
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02173

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/700,737
(B) FILING DATE: 15-AUG-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brook, David E.
(B) REGISTRATION NUMBER: 22,592
(C) REFERENCE/DOCKET NUMBER: LKS95-10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 861-6240
(B) TELEFAX: (617) 861-9540

(2) INFORMATION FOR SEQ ID NO:1:

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/700,737DATE: 12/18/96
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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 13..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTACKRGWMK WCATGRRATG SASCTRKRTC ATYYTCTTCT TGGTATCAAC AGCTACAAGT	60
GTCCACTCCC AGGTCCAAC GCAGCAGCCT GGGGCTGAGC TTGTGAAGCC TGGGACTTCA	120
GTGAAGCTGT CCTGCAAGGG TTATGGCTAC ACCTTCACCA GCTACTGGAT GCACTGGGTG	180
AAGCAGAGGC CTGGACAAGG CCTTGAGTGG ATCGGAGAGA TTGATCCTTC TGAGAGTAAT	240
ACTAACTACA ATCAAAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAT TTCCTCCAGC	300
ACAGCCTACA TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCGGTCTA CTATTGTGCA	360
AGAGGGGGTT ACGACGGATG GGAATATGCT ATTGACTACT GGGGTCAAGG CACCTCAGTC	420
ACCGTCTCCT CAGCCAAAAC GACACCRYCN CSYKTMTCYC YYSBDNNCCC YKGRWSCYTG	480
GNNGAAGCTT GGGA	494

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Phe	Leu	Val	Ser	Thr	Ala	Thr	Ser
1					5				10					15	
Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys

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	20	25	30
100			
101			
102	Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe		
103	35	40	45
104			
105	Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu		
106	50	55	60
107			
108	Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn		
109	65	70	75
110			
111	Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser		
112	85	90	95
113			
114	Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val		
115	100	105	110
116			
117	Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp		
118	115	120	125
119			
120	Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr		
121	130	135	140
122			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 18..428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

140	TTACTTGACG ACTCGGG ATG GGA TGG AGC TAT ATC ATC TTC TTC TTG GTA	50
141	Met Gly Trp Ser Tyr Ile Ile Phe Phe Leu Val	
142	1	5
143		
144	TCA ACA GCT ACA AGT GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG	98
145	Ser Thr Ala Thr Ser Val His Ser Gln Val Gln Leu Gln Gln Pro Gly	
146	15	20
147		
148	GCT GAG CTT GTG AAG CCT GGG ACT TCA GTG AAG CTG TCC TGC AAG GGT	146
149	Ala Glu Leu Val Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly	
150	30	35
151		40
152		

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153 TAT GGC TAC ACC TTC ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG      194
154 Tyr Gly Tyr Thr Phe Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg
155      45                      50                      55
156
157 CCT GGA CAA GGC CTT GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT      242
158 Pro Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser
159      60                      65                      70                      75
160
161 AAT ACT AAC TAC AAT CAA AAA TTC AAG GGC AAG GCC ACA TTG ACT GTA      290
162 Asn Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val
163      80                      85                      90
164
165 GAC ATT TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT      338
166 Asp Ile Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
167      95                      100                      105
168
169 GAG GAC TCT GCG GTC TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG      386
170 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp
171      110                      115                      120
172
173 GAC TAT GCT ATT GAC TAC TGG GGT CAA GGC ACA TCA GTC ACC      428
174 Asp Tyr Ala Ile Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
175      125                      130                      135
176
177
178 (2) INFORMATION FOR SEQ ID NO:4:
179
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 137 amino acids
182 (B) TYPE: amino acid
183 (D) TOPOLOGY: linear
184
185 (ii) MOLECULE TYPE: protein
186
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
188
189 Met Gly Trp Ser Tyr Ile Ile Phe Phe Leu Val Ser Thr Ala Thr Ser
190      1                      5                      10                      15
191
192 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
193      20                      25                      30
194
195 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
196      35                      40                      45
197
198 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
199      50                      55                      60
200
201 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
202      65                      70                      75                      80
203
204 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
205      85                      90                      95

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206
207 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
208 100 105 110
209
210 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
211 115 120 125
212
213 Tyr Trp Gly Gln Gly Thr Ser Val Thr
214 130 135
215
216 (2) INFORMATION FOR SEQ ID NO:5:
217
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 535 base pairs
220 (B) TYPE: nucleic acid
221 (C) STRANDEDNESS: double
222 (D) TOPOLOGY: linear
223
224
225
226 (ix) FEATURE:
227 (A) NAME/KEY: CDS
228 (B) LOCATION: 16..435
229
230
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
232
233 CGATTACTAG TCGAC ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG 51
234 Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu
235 140 145
236
237 TTC TGG ATT CCT GTT TCC GGA GGT GAT GTT GTG GTG ACT CAA ACT CCA 99
238 Phe Trp Ile Pro Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro
239 150 155 160 165
240
241 CTC TCC CTG CCT GTC AGC TTT GGA GAT CAA GTT TCT ATC TCT TGC AGG 147
242 Leu Ser Leu Pro Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg
243 170 175 180
244
245 TCT AGT CAG AGT CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG 195
246 Ser Ser Gln Ser Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp
247 185 190 195
248
249 TAC CTG CAC AAG CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT 243
250 Tyr Leu His Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile
251 200 205 210
252
253 TCC AAC AGA TTT TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA 291
254 Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
255 215 220 225
256
257 GGG ACA GAT TTC ACA CTC AAG ATC AGC ACA ATA AAG CCT GAG GAC TTG 339
258 Gly Thr Asp Phe Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu